

SEQUENCE LISTING

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98 SEP 11 PM 3:29

<110> Yuji, HATADA
Katsuya, OZAKI
Katsutoshi, ARA
Shuji, KAWAI
Susumu, ITO

<120> GENE ENCODING ALKALINE LIQUEFYING ALPHA-AMYLASE

<130> 2173-106P

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<160> 11

<170> PatentIn Ver. 2.0

<210> 1
<211> 1776
<212> DNA
<213> Bacillus sp.

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<221> CDS
<222> (145)..(1692)

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aaattgaagg agagggtgct tttt atg aaa ctt cat aac cgt ata att agc 171
Met Lys Leu His Asn Arg Ile Ile Ser
1 5

gta cta tta aca cta ttg tta gct gta gct gtt ttg ttt cca tat atg 219
Val Leu Leu Thr Leu Leu Ala Val Ala Val Leu Phe Pro Tyr Met
10 15 20 25

acg gaa cca gca caa gcc cat cat aat ggg acg aat ggg acc atg atg 267
Thr Glu Pro Ala Gln Ala His His Asn Gly Thr Asn Gly Thr Met Met
30 35 40

cag tat ttt gaa tgg cat ttg cca aat gac ggg aac cac tgg aac agg 315
Gln Tyr Phe Glu Trp His Leu Pro Asn Asp Gly Asn His Trp Asn Arg
45 50 55

tta cga gat gac gca gct aac tta aag agt aaa ggg att acc gct gtt			363
Leu Arg Asp Asp Ala Ala Asn Leu Lys Ser Lys Gly Ile Thr Ala Val			
60	65	70	
tgg att cct cct gca tgg aag ggg act tcg caa aat gat gtt ggg tat			411
Trp Ile Pro Pro Ala Trp Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr			
75	80	85	
ggt gcc tat gat ttg tac gat ctt ggt gag ttt aac caa aag gga acc			459
Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr			
90	95	100	105
gtc cgt aca aaa tat ggc aca agg agt cag ttg caa ggt gcc gtg aca			507
Val Arg Thr Lys Tyr Gly Thr Arg Ser Gln Leu Gln Gly Ala Val Thr			
110	115	120	
tct ttg aaa aat aac ggg att caa gtt tat ggg gat gtc gtg atg aat			555
Ser Leu Lys Asn Asn Gly Ile Gln Val Tyr Gly Asp Val Val Met Asn			
125	130	135	
cat aaa ggt gga gca gac ggg aca gag atg gta aat gcg gtg gaa gtg			603
His Lys Gly Gly Ala Asp Gly Thr Glu Met Val Asn Ala Val Glu Val			
140	145	150	
aac cga agc aac cga aac caa gaa ata tca ggt gaa tac acc att gaa			651
Asn Arg Ser Asn Arg Asn Gln Glu Ile Ser Gly Glu Tyr Thr Ile Glu			
155	160	165	
gca tgg acg aaa ttt gat ttc cct gga aga gga aat acc cat tcc aac			699
Ala Trp Thr Lys Phe Asp Phe Pro Gly Arg Gly Asn Thr His Ser Asn			
170	175	180	185
ttt aaa tgg cgc tgg tat cat ttt gat ggg aca gat tgg gat cag tca			747
Phe Lys Trp Arg Trp Tyr His Phe Asp Gly Thr Asp Trp Asp Gln Ser			
190	195	200	
cgt cag ctt cag aac aaa ata tat aaa ttc aga ggt acc gga aag gca			795
Arg Gln Leu Gln Asn Lys Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala			
205	210	215	
tgg gac tgg gaa gta gat ata gag aac ggc aac tat gat tac ctt atg			843
Trp Asp Trp Glu Val Asp Ile Glu Asn Gly Asn Tyr Asp Tyr Leu Met			
220	225	230	
tat gca gac att gat atg gat cat cca gaa gta atc aat gaa ctt aga			891
Tyr Ala Asp Ile Asp Met Asp His Pro Glu Val Ile Asn Glu Leu Arg			
235	240	245	

aat tgg gga gtt tgg tat aca aat aca ctt aat cta gat gga ttt aga 939
 Asn Trp Gly Val Trp Tyr Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg
 250 255 260 265

atc gat gct gtg aaa cat att aaa tac agc tat acg aga gat tgg cta 987
 Ile Asp Ala Val Lys His Ile Lys Tyr Ser Tyr Thr Arg Asp Trp Leu
 270 275 280

aca cat gtg cgt aac acc aca ggt aaa cca atg ttt gca gtt gca gaa 1035
 Thr His Val Arg Asn Thr Gly Lys Pro Met Phe Ala Val Ala Glu
 285 290 295

ttt tgg aaa aat gac ctt gct gca atc gaa aac tat tta aat aaa aca 1083
 Phe Trp Lys Asn Asp Leu Ala Ala Ile Glu Asn Tyr Leu Asn Lys Thr
 300 305 310

agt tgg aat cac tcc gtg ttc gat gtt cct ctt cat tat aat ttg tac 1131
 Ser Trp Asn His Ser Val Phe Asp Val Pro Leu His Tyr Asn Leu Tyr
 315 320 325

aat gca tct aat agt ggt ggc tat ttt gat atg aga aat att tta aat 1179
 Asn Ala Ser Asn Ser Gly Gly Tyr Phe Asp Met Arg Asn Ile Leu Asn
 330 335 340 345

ggt tct gtc gta caa aaa cac cct ata cat gca gtc aca ttt gtt gat 1227
 Gly Ser Val Val Gln Lys His Pro Ile His Ala Val Thr Phe Val Asp
 350 355 360

aac cat gac tct cag cca gga gaa gca ttg gaa tcc ttt gtt caa tcg 1275
 Asn His Asp Ser Gln Pro Gly Glu Ala Leu Glu Ser Phe Val Gln Ser
 365 370 375

tgg ttc aaa cca ctg gca tat gca ttg att ctg aca agg gag caa ggt 1323
 Trp Phe Lys Pro Leu Ala Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly
 380 385 390

tac cct tcc gta ttt tac ggt gat tac tac ggt ata cca act cat ggt 1371
 Tyr Pro Ser Val Phe Tyr Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly
 395 400 405

gtt cct tcg atg aaa tct aaa att gat cca ctt ctg cag gca cgt caa 1419
 Val Pro Ser Met Lys Ser Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln
 410 415 420 425

acg tat gcc tac gga acc caa cat gat tat ttt gat cat cat gat att 1467
 Thr Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe Asp His His Asp Ile
 430 435 440

atc ggc tgg acg aga gaa ggg gac agc tcc cac cca aat tca gga ctt 1515
 Ile Gly Trp Thr Arg Glu Gly Asp Ser Ser His Pro Asn Ser Gly Leu
 445 450 455

gca act att atg tcc gat ggg cca ggg ggt aat aaa tgg atg tat gtc 1563
 Ala Thr Ile Met Ser Asp Gly Pro Gly Asn Lys Trp Met Tyr Val
 460 465 470

ggg aaa cat aaa gct ggc caa gta tgg aga gat atc acc gga aat agg 1611
 Gly Lys His Lys Ala Gly Gln Val Trp Arg Asp Ile Thr Gly Asn Arg
 475 480 485

tct ggt acc gtc acc att aat gca gat ggt tgg ggg aat ttc act gta 1659
 Ser Gly Thr Val Thr Ile Asn Ala Asp Gly Trp Gly Asn Phe Thr Val
 490 495 500 505

aac gga ggg gca gtt tcg gtt tgg gtg aag caa taaataagga acaagaggcg 1712
 Asn Gly Gly Ala Val Ser Val Trp Val Lys Gln
 510 515

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<213> Bacillus sp.

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His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His Leu
 35 40 45

Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala Asn
 50 55 60

Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp Lys
 65 70 75 80

Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp

85

90

95

Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr
 100 105 110

Arg Ser Gln Leu Gln Gly Ala Val Thr Ser Leu Lys Asn Asn Gly Ile
 115 120 125

Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp Gly
 130 135 140

Thr Glu Met Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn Gln
 145 150 155 160

Glu Ile Ser Gly Glu Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp Phe
 165 170 175

Pro Gly Arg Gly Asn Thr His Ser Asn Phe Lys Trp Arg Trp Tyr His
 180 185 190

Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys Ile
 195 200 205

Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp Ile
 210 215 220

Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met Asp
 225 230 235 240

His Pro Glu Val Ile Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr Thr
 245 250 255

Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His Ile
 260 265 270

Lys Tyr Ser Tyr Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr Thr
 275 280 285

Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu Ala
 290 295 300

Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val Phe
 305 310 315 320

Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly Gly
 325 330 335

Tyr Phe Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys His

340

345

350

Pro Ile His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro Gly
 355 360 365

Glu Ala Leu Glu Ser Phe Val Gln Ser Trp Phe Lys Pro Leu Ala Tyr
 370 375 380

Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr Gly
 385 390 395 400

Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ser Met Lys Ser Lys
 405 410 415

Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Tyr Ala Tyr Gly Thr Gln
 420 425 430

His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu Gly
 435 440 445

Asp Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp Gly
 450 455 460

Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys His Lys Ala Gly Gln
 465 470 475 480

Val Trp Arg Asp Ile Thr Gly Asn Arg Ser Gly Thr Val Thr Ile Asn
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Trp Val Lys Gln
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